From:	Sullivan, Daniel
Sent:	Thursday, December 30, 2004 12:29 PM
To:	STIC-Biotech/ChemLib
Subject:	Request 09963803

Please search for the following in the pending, issued patent and commercial databases.

A nucleic acid comprising SEQ ID NO: 2

Thank you.

CRFB

Daniel M. Sullivan

Examiner AU 1636
Remsen Bldg.
Room 2A74

Tel: (571) 272-0779

Mailbox: 2C70

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: January 5, 2005, 00:39:34 ; Search time 2589 Seconds
(without alignments)
7248.537 Million cell updates/sec

Title: US-09-963-803-2
Perfect score: 515
Sequence: 1 ccagaaggtaattaccaag.........cagagaaattgtaagttg 515

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821985908 residues
Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
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9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	62	12.0	537	8	AZ702081	AZ702081 RPCI-23-2
	2	62	12.0	540	8	AZ032908	AZ032908 RPCI-23-3
c	3	61.8	12.0	997	8	CNS005TE	CNS005TE Drosophil
c	4	59.8	11.6	629	9	CB010465	CB010465 Tetraodon
	5	59.6	11.6	625	9	CE633607	CE633607 tigr-gss-
c	6	59.2	11.5	683	9	CE830234	CE830234 tigr-gss-
c	7	59.2	11.5	1101	9	CNS0021J	CNS0021J Drosophil
c	8	58.8	11.4	907	9	CNS02IJ4	CNS02IJ4 Tetraodon
c	9	58.2	11.3	416	8	AL176953	AL176953 Tetraodon
	10	58	11.3	336	8	AZ652793	AZ652793 1M052610
c	11	58	11.3	432	8	AZ635799	AZ635799 1M0493L08
c	12	58	11.3	981	1	CE704975	CE704975 tigr-gss-
c	13	57.2	11.1	473	8	AL564376	AL564376 AL564376
	14	57.2	11.1	756	9	AZ891439	AZ891439 RPCI-24-1
c	15	57.2	11.1	775	9	AG602876	AG602876 Mus muscu
c	16	57	11.1	769	9	AG464079	AG464079 Mus muscu
	17	56.6	11.0	707	8	AZ985865	AZ985865 2M0267C20
	18	56.4	11.0	571	9	CE097846	CE097846 tigr-gss-
	19	56.4	11.0	1250	9	AG310954	AG310954 Mus muscu
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	21	56.2	10.9	681	9	CE197701	CE197701 tigr-gss-
c	22	56.2	10.9	877	9	CR253706	CR253706 Forward 8
c	23	56	10.9	486	9	CE764895	CE764895 tigr-gss-
	24	56	10.9	639	9	CNS0170D	CNS0170D Drosophil
	25	56	10.9	666	6	BY751847	BY751847 BY751847
	26	55.8	10.9	1008	6	CL059735	CL059735 CH216-90J
	27	55.8	10.8	1101	6	CNS00LT2	CNS00LT2 Drosophil
	28	55.6	10.8	920	8	AL078714	AL078714 Drosophil
	29	55.4	10.8	733	8	AZ691914	AZ691914 ENTMU26TR
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	32	55.2	10.7	1187	8	AG405712	AG405712 Mus muscu
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	34	55	10.7	298	8	AG280488	AG280488 Mus muscu
	35	55	10.7	519	8	CE521047	CE521047 tigr-gss-
	36	55	10.7	606	9	BH062219	BH062219 RPCI-24-3
	37	55	10.7	625	8	CE451752	CE451752 tigr-gss-
	38	55	10.7	667	8	AZ912416	AZ912416 RPCI-24-1
	39	55	10.7	675	9	AZ600028	AZ600028 1M041609
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c	43	54.8	10.6	776	8	BH040136	BH040136 RPCI-24-2
c	44	54.6	10.6	551	8	BH044827	BH044827 RPCI-24-2
c	45	54.6	10.6	614	9	CE136192	CE136192 tigr-gss-
					9	CE524492	CE524492 tigr-gss-

ALIGNMENTS

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           RPCI-23-234D14, genomic survey sequence.   537 bp   DNA   linear   GSS 24-JAN-2001

LOCUS   AZ702081   537 bp   DNA   linear   GSS 24-JAN-2001
DEFINITION RPCI-23-234D14.TV RPCI-23 Mus musculus genomic clone
            RPCI-23-234D14, genomic survey sequence.
ACCESSION   AZ702081
VERSION   AZ702081.1 GI:12425141
KEYWORDS   GSS.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 537)
  AUTHORS   Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
            Akinret,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de
            Jong,P. and Fraser,C.M.
  TITLE   Mouse BAC End Sequences from Library RPCI-23
  JOURNAL   Unpublished (1999)
COMMENT   Other_GSSs: RPCI-23-234D14.TJ
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-23. For BAC
            library availability, please contact Pieter de Jong
            (pdejong@mail.cho.org). Clones may be purchased from BACPAC
            Resources (http://www.chori.org/bacpac/orderingframe.html). BAC end
            page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Other_GSSs: http://www.tigr.org/tdb/bac_ends/mouse/bac_ends.html
            Seq primer: T7
            Plate: 234 row: D column: 14
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                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPCI-23-234D14"
                     /sex="Female"
                     /lab_host="DH10B"
                     /clone_lib="RPCI-23"
                     /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
                     EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
                     brain genomic DNA was isolated and partially digested

OM nucleic - nucleic search, using sw model

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Run on: January 5, 2005, 00:56:14 ; Search time 437 Seconds
(without alignments)
6656.411 Million cell updates/sec

Title: US-09-963-803-2
Perfect score: 515
Sequence: 1 ccagaaggtaattatccaag..........cagagaaattgtaagttg 515

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4176236 seqs, 282412795 residues

Total number of hits satisfying chosen parameters: 8352472

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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7: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	515	100.0	1839	16	US-10-415-302-19	Sequence 19, Appl
4	515	100.0	4677	16	US-10-415-302-21	Sequence 21, App

ALIGNMENTS

13	120.6	23.4	392	10	US-09-963-803-21	Sequence 21, Appl
14	120.6	23.4	393	10	US-09-963-803-19	Sequence 19, Appl
15	120.6	23.4	462	10	US-09-963-803-20	Sequence 20, Appl
16	120.6	23.4	600	10	US-09-963-803-22	Sequence 22, Appl
17	120.6	23.4	9285	10	US-09-845-064-52	Sequence 52, Appl
18	120.6	23.4	15077	10	US-09-845-064-57	Sequence 57, Appl
19	113	21.9	604	10	US-09-963-803-23	Sequence 23, Appl
20	110.8	21.5	301	10	US-09-963-803-7	Sequence 7, Appli
21	110.8	21.5	348	10	US-09-963-803-4	Sequence 4, Appli
22	110.8	21.5	398	10	US-09-963-803-6	Sequence 6, Appli
23	108.4	21.0	472	10	US-09-963-803-25	Sequence 25, Appl
24	108.4	21.0	541	10	US-09-963-803-24	Sequence 24, Appl
25	62	12.0	62	10	US-09-963-803-10	Sequence 10, Appl
c 26	57	11.1	224412	17	US-10-322-281-115	Sequence 115, App
c 27	56.8	11.0	289190	17	US-10-012-600B-105	Sequence 105, App
c 28	56.2	10.9	948	14	US-10-674-124A-5858	Sequence 5858, Ap
c 29	55	10.7	472	18	US-10-087-192-451	Sequence 451, App
c 30	54	10.5	256525	13	US-09-864-761-18143	Sequence 18143, A
c 31	52.6	10.2	298	9	US-10-723-860-4422	Sequence 4422, Ap
c 32	51.8	10.1	131673	18	US-09-764-853-14888	Sequence 14888, A
c 33	51.4	10.0	336	18	US-10-027-632-127627	Sequence 127627,
c 34	51.4	10.0	609	13	US-10-027-632-127627	Sequence 127627,
c 35	51.4	10.0	609	15	US-10-027-332-127627	Sequence 127627,
c 36	51.2	9.9	563	18	US-10-357-930-50743	Sequence 50743, A
c 37	51.2	9.9	803	17	US-10-437-963-72176	Sequence 72176, A
c 38	51	9.9	8895	9	US-09-764-853-887	Sequence 887, App
c 39	51	9.9	8895	9	US-09-764-853-937	Sequence 937, App
c 40	51	9.9	8895	14	US-10-091-438-250	Sequence 250, App
c 41	51	9.9	8895	14	US-10-091-438-256	Sequence 256, App
c 42	51	9.9	8895	14	US-10-091-438-246	Sequence 246, App
c 43	51	9.9	9656	9	US-10-091-438-255	Sequence 933, App
c 44	51	9.9	9656	14	US-10-091-438-255	Sequence 246, App
c 45	51	9.9	9656	14	US-10-091-438-255	Sequence 255, App

RESULT 1
US-09-963-803-2
Sequence 2, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yello
TITLE OF INVENTION: virus and cassava vein mosaic virus
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1

SEQ ID NO 2
LENGTH: 515
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Promoter from the intergenic region of Cassava Vein Mosaic vi
OTHER INFORMATION: of 515 bp in length EMBL
FEATURE:
NAME/KEY: promoter
LOCATION: (1)..(515)
OTHER INFORMATION:
US-09-963-803-2

OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 01:00:34 ; Search time 87 Seconds
                                                     (without alignments)
                         Copyright (c) 1993 - 2005 Compugen Ltd.
                         GenCore version 5.1.6
                                                     4207.543 Million cell updates/sec

Title: US-09-963-803-2
Perfect score: 515
Sequence: 1 ccagaaggtaattatccaag.........cagagaaatttgtaagttg 515
Scoring table: ,
Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0
Searched: 824507 seqs, 35394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
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3	511.8	99.4	853	4	US-09-641-466-2	Sequence 2, Appli
4	511.8	99.4	12241	4	US-09-948-138-4	Sequence 4, Appli
5	511.4	99.3	8340	4	US-09-847-057-4	Sequence 4, Appli
6	427	82.9	8340	4	US-09-874-926-4	Sequence 4, Appli
7	427	82.9	593	4	US-09-641-466-3	Sequence 3, Appli
8	427	82.9	857	4	US-09-641-466-4	Sequence 4, Appli
9	332	64.5	931	4	US-09-641-466-5	Sequence 5, Appli
10	332	64.5	931	4	US-09-641-466-6	Sequence 6, Appli
11	332	64.5	931	4	US-09-641-466-6	Sequence 6, Appli
12	76	14.8	7218	1	US-08-232-463-14	Sequence 14, Appli
13	44.6	8.7	3279	3	US-08-446-137B-1	Sequence 1, Appli
14	43.8	8.5	152331	4	US-09-128-155-16	Sequence 16, Appli
15	43.2	8.4	929	4	US-09-671-317-14	Sequence 14, Appl
16	43.2	8.4	1001	4	US-09-671-317-439	Sequence 439, Appl
17	42.8	8.3	106746	4	US-09-326-402C-1	Sequence 1, Appli
18	42.8	8.3	106746	4	US-09-326-402C-12	Sequence 12, Appli
19	42.6	8.3	5433	3	US-08-229-329-1	Sequence 1, Appli
20	42.4	8.2	5455	4	US-10-204-708-34	Sequence 34, Appli
21	42.2	8.2	478	4	US-09-521-976-10407	Sequence 10407, A
22	42.2	8.2	696	3	US-09-461-697-193	Sequence 193, App
23	42.2	8.2	699	3	US-09-461-697-191	Sequence 191, App
24	42.2	8.2	717	3	US-09-461-697-189	Sequence 189, App
25	42.2	8.2	774	3	US-09-461-697-187	Sequence 187, App
26	42.2	8.2	819	3	US-09-461-697-185	Sequence 185, App
27	42.2	8.2	176373	3	US-09-128-155-17	Sequence 17, Appl
28	41.4	8.0	1359	4	US-09-248-796A-1541	Sequence 1541, Ap
29	41.2	8.0	188	1	US-08-115-497-21	Sequence 21, Appli
30	41.2	8.0	188	3	US-08-466-670-21	Sequence 21, Appli
31	41.2	8.0	188	2	US-08-291-011-1	Sequence 1, Appli
32	41.2	8.0	188	1	US-09-266-055-1	Sequence 1, Appli
33	41.2	8.0	188	4	US-09-935-247-1	Sequence 1, Appli
34	41.2	8.0	405	2	US-08-299-074A-1	Sequence 1, Appli
35	41.2	8.0	405	3	US-09-399-773-1	Sequence 1, Appli
36	41.2	8.0	843	4	US-09-248-796A-5393	Sequence 5393, Ap
37	41.2	8.0	1434	4	US-09-248-796A-5873	Sequence 5873, Ap
38	41.2	8.0	1437	3	US-09-446-504-63	Sequence 63, Appli
39	41.2	8.0	1437	3	US-09-712-266-63	Sequence 63, Appli
40	41.2	8.0	2223	1	US-08-257-073-4	Sequence 4, Appli
41	41.2	8.0	3211	2	US-08-574-959A-8	Sequence 8, Appli
42	41.2	8.0	3211	3	US-09-357-014-8	Sequence 8, Appli
43	41.2	8.0	3574	3	US-09-446-504-83	Sequence 83, Appl
44	41.2	8.0	3574	3	US-09-712-266-83	Sequence 83, Appl
45	41.2	8.0	3901	2	US-08-574-959A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-641-466-1

; Sequence 1, Application US/09641466
; Patent No. 6664384
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; APPLICANT: Nielsen, Mark T.
; TITLE OF INVENTION: Duplicated Cassava Vein Mosaic Virus
; TITLE OF INVENTION: Enhancers and Uses Thereof
; FILE REFERENCE: 07678/078002
; CURRENT APPLICATION NUMBER: US/09/641,466
; CURRENT FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 1
; LENGTH: 515
; TYPE: DNA
; ORGANISM: cassava vein mosaic virus
US-09-641-466-1

Query Match   99.7%; Score 513.4; DB 4; Length 515;
Best Local Similarity   99.8%; Pred. No. 4.6e-124; Matches 514; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db   1 CCAGAAGGTAATTATCCAAGATGTAGCCATCAAGAATCCAAATGTTTACGGGGAAAAACTATG 60

Qy   61 GAAGTATTATGTGAGCTCAGCGAAGAAGCAGATCAATCAATATGCAAACCTTATGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GAAGTATTATGTGAGCTCAGCGAAGAAGCAGATCAATCAATATGCAAACCTTATGT 120

Qy   121 TCAAAAAATGAAGAAGTTACAGATACAAGATCCTATACTGCCAGAATACGAAGAAGAAGAATAC 180
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Db   121 TCAAAAAATGAAGAAGTTACAGATACAAGATCCTATACTGCCAGAATACGAAGAAGAAGAATAC 180

Qy   181 GTAGAAAATTGAAAAAAGAAGAACCAGGCGAAGAGAAAAGAAATCTTGAAGACGTAAGCACTGAC 240
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Db   181 GTAGAAAATTGAAAAAAGAAGAACCAGGCGAAGAGAAAAGAAATCTTGAAGACGTAAGCACTGAC 240

Qy   241 GACAACAATGAAAAAGAAGAGAGATAAGGTCGGTGAGTTGAAAGAGACATAGAGAGACACAT 300
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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 00:38:49

Title: US-09-963-803-2
Perfect score: 515
Sequence: 1 ccagaaggtaattatccaag.........cagagaaattgtaagttg 515

Scoring table: IDENTITY_NUC
              Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269972

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Databases :
1: N_Geneseq_23Sep04:*
2: geneseqn1980s:*
3: geneseqn1990s:*
4: geneseqn2000s:*
5: geneseqn2001as:*
6: geneseqn2001bs:*
7: geneseqn2002as:*
8: geneseqn2002bs:*
9: geneseqn2003as:*
10: geneseqn2003bs:*
11: geneseqn2003cs:*
12: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	515	100.0	515	3	AAA96836	Aaa96836 Promoter
2	515	100.0	532	4	AAD11575	Aad11575 Cassava V
3	515	100.0	538	12	ADO85792	Ado85792 Promoter
4	515	100.0	538	12	ADO59549	Ado59549 pSP29 vec
5	515	100.0	538	12	ADO54812	Ado54812 Cassava v
6	515	100.0	1839	6	ABL57988	Abl57988 4-Hydroxy
7	515	100.0	4677	6	ABL57989	Abl57989 4-Hydroxy
8	515	100.0	8187	6	ABL58082	Abl58082 4-Hydroxy
9	515	99.8	1052	6	ABS53107	Abs53107 Transgene
10	514	99.8	1590	6	ABS53109	Abs53109 Transgene
11	514	99.7	1590	6	AAF55505	Aaf55505 Nucleotid
12	513.4	99.7	524	2	AAV14020	Aav14020 CsVMV pro
13	513.4	99.7	526	2	AAV14018	Aav14018 CsVMV pro
14	513.4	99.7	853	4	AAF55506	Aaf55506 Nucleotid
15	513.4	99.4	12241	6	AAD36732	Aad36732 Binary ve
16	511.8	99.4	12241	6	ABG73049	Abg73049 Tomato an
17	511.8	99.4	12241	11	ADO05418	Ado05418 Binary ve
18	511.8	99.3	8340	6	AAD24139	Aad24139 pAGI4002
19	511.4	99.3	8340	6	ABA04755	Aba04755 Binary ve
20	461	89.5	1590	6	ABS53109	Abs53109 Transgene
21	431.8	83.8	491	2	AAV14030	Aav14030 CsVMV pro
22	427	82.9	593	4	AAF55507	Aaf55507 Nucleotid
23	427	82.9	857	4	AAF55508	Aaf55508 Nucleotid
24	427	82.9	931	4	AAF55509	Aaf55509 Nucleotid
25	412.2	80.0	482	2	AAV14027	Aav14027 CsVMV pro
26	401.8	78.0	476	2	AAV14053	Aav14053 CsVMV pro
27	401.2	77.9	411	2	AAV14021	Aav14021 CsVMV pro
28	392	76.1	392	2	AAV14019	Aav14019 CsVMV pro
29	390.2	75.8	710	12	ADO59550	Ado59550 Double Cs
30	390.2	75.8	710	12	ADO54813	Ado54813 Cassava v
31	385.8	74.9	468	2	AAV14029	Aav14029 CsVMV pro
32	365.8	71.0	458	2	AAV14028	Aav14028 CsVMV pro
33	333.4	64.7	441	2	AAV14033	Aav14033 CsVMV pro
34	332	64.5	931	4	AAF55510	Aaf55510 Nucleotid
35	332	64.5	931	4	AAF55510	Aaf55510 Nucleotid
36	300.4	58.3	420	2	AAV14026	Aav14026 CsVMV pro
37	295.2	57.3	418	2	AAV14022	Aav14022 CsVMV pro
38	285.8	55.5	408	2	AAV14032	Aav14032 CsVMV pro
39	265.8	51.6	408	2	AAV14031	Aav14031 CsVMV pro
40	250.2	48.6	261	2	AAV14023	Aav14023 CsVMV pro
41	219	42.5	219	12	ADO59546	Ado59546 Cassava v
42	219	42.5	219	2	ADO54809	Ado54809 Cassava v
43	219	42.5	1052	6	ABS53107	Abs53107 Transgene
44	194	37.7	1618	6	ABS53117	Abs53117 Transgene
45	194	37.7	1618	6	ABS53117	Abs53117 Transgene

ALIGNMENTS

RESULT 1
AAA96836

ID   AAA96836 standard; DNA; 515 BP.
XX
AC   AAA96836;
XX
DT   19-FEB-2001 (first entry)
XX
DE   Promoter from intergenic region of Cassava vein mosaic virus.
XX
KW   Promoter; intergenic region; Commelina yellow mottle virus;
KW   chimeric expression promoter; plant vascular expression promoter;
KW   plant green tissue expression promoter; Cassava vein mosaic virus;
KW   transgenic plant; ss.
XX
OS   Cassava vein mosaic virus.
XX
PN   WO200058485-A1.
XX
PD   05-OCT-2000.
XX
PF   29-MAR-2000; 2000WO-IB000370.
XX
PR   29-MAR-1999; 99FR-00003925.
XX
PA   (MERI-) MERISTEM THERAPEUTICS.
XX
PI   Rance I, Gruber V, Theisen M;
XX
DR   WPI; 2000-647238/62.
XX
PT   Chimeric expression promoter for transgenic plant production, comprises
PT   sequence from promoter comprising vascular expression region replaced
PT   with sequence from promoter comprising green tissue expression region.
XX
PS   Claim 4; Page 80; 91pp; English.
XX
CC   The present sequence represents a promoter fragment from the intergenic
CC   region of Cassava vein mosaic virus. The promoter is used to construct
CC   chimeric expression promoters. These chimeric promoters comprise a
CC   nucleic acid sequence which is derived from a first plant promoter, in
CC   which a plant vascular expression promoter region is replaced with a
CC   nucleic acid sequence derived from a second plant promoter comprising a
CC   plant green tissue expression promoter region. Preferably, the first

QM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: January 5, 2005, 00:54:44 ; Search time 2765 Seconds
(without alignments)
8808.027 Million cell updates/sec

Title: US-09-963-803-2
Perfect score: 515
Sequence: 1 ccagaaggtaattatccaag.........caggaaattgtaagttg 515

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 4526729 seqs, 2364849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	515	100.0	515	6	BD262203	BD262203 Chimeric
2	515	100.0	515	6	AX036736	AX036736 Sequence
3	515	100.0	532	6	AX202413	AX202413 Sequence
4	515	100.0	538	6	CQ828123	CQ828123 Sequence
5	515	100.0	538	6	CQ828192	CQ828192 Sequence
6	515	100.0	538	6	CQ830297	CQ830297 Sequence
7	515	100.0	838	6	BD205013	BD205013 Gene enco
8	515	100.0	838	6	AX014764	AX014764 Sequence
9	515	100.0	838	6	BD205014	BD205014 Gene enco
10	515	100.0	1036	6	AX014765	AX014765 Sequence
11	515	100.0	8158	14	CVU20341	U20341 Cassava vei
12	515	100.0	8159	14	CVU59751	U59751 Cassava vei
13	513.4	99.7	515	6	AR439662	AR439662 Sequence
14	513.4	99.7	515	6	AX088388	AX088388 Sequence
15	513.4	99.7	515	6	AR439663	AR439663 Sequence
16	513.4	99.7	853	6	AX088389	AX088389 Sequence
17	511.8	99.7	12241	6	AX412168	AX412168 Sequence
18	511.4	99.3	8340	6	AR275735	AR275735 Sequence
19	511.4	99.3	8340	6	AR321647	AR321647 Sequence
20	511.4	99.3	8340	6	AX329231	AX329231 Sequence
21	511.4	99.3	8340	6	AX338536	AX338536 Sequence
22	427	82.9	593	6	AR439664	AR439664 Sequence
23	427	82.9	593	6	AX088390	AX088390 Sequence
24	427	82.9	857	6	AR439665	AR439665 Sequence
25	427	82.9	931	6	AX088391	AX088391 Sequence
26	427	82.9	931	6	AR439666	AR439666 Sequence
27	427	82.9	931	6	AX088392	AX088392 Sequence
28	390.2	75.8	710	6	CQ828124	CQ828124 Sequence
29	390.2	75.8	710	6	CQ828193	CQ828193 Sequence
30	332	64.5	931	6	AR439667	AR439667 Sequence
31	332	64.5	931	6	AX088393	AX088393 Sequence
32	332	64.5	931	6	AX088120	AX088120 Sequence
33	332	64.5	931	6	CQ828189	CQ828189 Sequence
34	219	42.5	219	6	CQ828120	CQ828120 Sequence
35	219	42.5	219	6	CQ828121	CQ828121 Sequence
36	168	32.6	168	6	CQ828190	CQ828190 Sequence
37	168	32.6	168	6	CQ828122	CQ828122 Sequence
38	126	24.5	168	6	CQ828122	CQ828122 Sequence
39	126	24.5	127	6	CQ828191	CQ828191 Sequence
40	125.8	24.4	317	6	BD262204	BD262204 Chimeric
41	125.8	24.4	317	6	AX036737	AX036737 Sequence
42	125.8	24.4	371	6	BD262206	BD262206 Chimeric
43	125.8	24.4	371	6	AX036739	AX036739 Sequence
44	120.6	23.4	392	6	BD262222	BD262222 Chimeric
45	120.6	23.4	392	6	AX036755	AX036755 Sequence

ALIGNMENTS

RESULT 1
BD262203
LOCUS   BD262203   515 bp   DNA   linear   PAT 17-JUL-2003
DEFINITION   Chimeric expression promoters originating from commelina yellow
             mottle virus and Cassava vein mosaic virus.
ACCESSION   BD262203
VERSION   BD262203.1 GI:33071971
KEYWORDS   JP 2002539837-A/2.
SOURCE   synthetic construct
  ORGANISM   synthetic construct
             artificial sequences.
REFERENCE   1 (bases 1 to 515)
  AUTHORS   Rance,I., Gruber,V. and Theisen,M.
  TITLE   Chimeric expression promoters originating from commelina yellow
             mottle virus and Cassava vein mosaic virus
  JOURNAL   Patent: JP 2002539837-A 2 26-NOV-2002;
             MERISTEM THERAPEUTICS
COMMENT   OS   Artificial Sequence
             PN   JP 2002539837-A/2
             PD   26-NOV-2002
             PF   29-MAR-2000 JP 2000608764
             PR   29-MAR-1999 FR   99/03925
             PI   IANN RANCE, VERONIQUE GRUBER, MANFRED THEISEN
             PC   C12N15/09,A01H5/00,C12N5/10,C12N5/00,C12N5/00 CC
             PC   from the intergenic region of Cassava Vein Mosaic CC
             PC   virus of 515 bp
             CC   in length EMBL U59751
             FH   Key   Location/Qualifiers
             FT   promoter   (1)..(515).
FEATURES   Location/Qualifiers
     source   1..515
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

Qy   Query Match   100.0%; Score 515; DB 6; Length 515;
              Best Local Similarity 100.0%; Pred. No. 6.2e-100;
              Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CCAGAAGGTAATTATCCAAGAGATGTAGCATCAAGAATCCAATGTTTACGGGAAAAACTATG 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||